

INTHE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of

Dan L. Eaton et al.

Serial No. 08/423,194

Filed: 18 April 1995

For: MPL LIGAND

Group Art Unit: 1812

Examiner: Unassigned

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envolupe addressed to Commissioner of Patents and Trademerks, Washington, D.C. 20231 on

(Date of Papositi

Name of Dapositing Party

9999

Date of Signature

CERTIFICATE RE: SEQUENCE LISTING

)

BOX SEQUENCE
Honorable Commissioner of Patents
and Trademarks
Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the content of the paper and computer readable copies are the same.

Date: September 8, 1995

460 Pt. San Bruno Blvd.

So. San Francisco, CA 94080-4990

Phone: (415) 225-1249 Fax: (415) 952-9881 Respectfully submitted,

Paryl B Winter Reg. No. 32,637

			353
-	\	(1) GEN	1005 SEQUENCE LISTING NERAL INFORMATION:
o .'	5	(i)	APPLICANT: Eaton, Dan L. de Sauvage, Frederic J.
hi	γ' / .	(ii)	TITLE OF INVENTION: MPL LIGAND
/	10	(iii)	NUMBER OF SEQUENCES: 77
/	15	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Genentech, Inc. (B) STREET: 460 Point San Bruno Blvd (C) CITY: South San Francisco (D) STATE: California (E) COUNTRY: USA (F) ZIP: 94080
	20	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: patin (Genentech)
•	25 30	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: 08/423194 (B) FILING DATE: 18 APR-1995 (C) CLASSIFICATION:
λ	30	(vii)	PRIOR APPLICATION DATA (A) APPLICATION NUMBER: 08/249376 (B) FILING DATE: 25-MAY-1994
	35	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/223263 (B) FILING DATE: 04-APR-1994
	40	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/196689 (B) FILING DATE: 15-FEB-1994
	45	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/185607 (B) FILING DATE: 21-JAN-1994
	50	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/176553 (B) FILING DATE: 03-JAN-1994
		(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Winter, Daryl B.

-104-

(B) REGISTRATION NUMBER: 32,637 (C) REFERENCE/DOCKET NUMBER: 871P4D2 (ix)TELECOMMUNICATION INFORMATION: 5 (A) TELEPHONE: 415/225-1249 (B) TELEFAX: 415/952-9881 (C) TELEX: 910/371-7168 (2) INFORMATION FOR SEQ ID NO:1: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: Met Glu Leu Thr Œlu Leu Leu Val Val Met Leu Leu Leu Thr -21 -20 -15 -10 Ala Arg Leu Thr Leu\Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser 25 Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val 25 30 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln 30 Met Glu Glu Thr Lys Ala Gln App Ile Leu Gly Ala Val Thr Leu 35 Leu Leu Glu Gly Val Met Ala Ala \Arg Gly Gln Leu Gly Pro Thr 70 Cys Leu Ser Ser Leu Leu Gly Gln Let Ser Gly Gln Val Arg Leu 40 Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro 105 110 45 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu 115 Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu 130 135 50 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr

155

150

	Alb 160	Val	Pro	Ser	Arg	Thr 165	Ser	Leu	Val	Leu	Thr 170	Leu	Asn	Glu	Leu
5	Pro 175	Asn	Arg	Thr	Ser	Gly 180	Leu	Leu	Glu	Thr	Asn 185	Phe	Thr	Ala	Ser
	Ala 190	Arg	Thr	Thr	Gly	Ser 195	Gly	Leu	Leu	Lys	Trp 200	Gln	Gln	Gly	Phe
10	Arg 205	Ala	Lye	Ile	Pro	Gly 210	Leu	Leu	Asn	Gln	Thr 215	Ser	Arg	Ser	Leu
15	Asp 220	Gln	Ile	Pro	Gly	Tyr 225	Leu	Asn	Arg	Ile	His 230	Glu	Leu	Leu	Asn
15	Gly 235	Thr	Arg	Gly	Leu	Phe 240	Pro	Gly	Pro	Ser	Arg 245	Arg	Thr	Leu	Gly
20	Ala 250	Pro	Asp	Ile	Sex	Ser 255	Gly	Thr	Ser	Asp	Thr 260	Gly	Ser	Leu	Pro
8, 7	Pro 265	Asn	Leu	Gln	Pro	Gly 270	Tyr	Ser	Pro	Ser	Pro 275	Thr	His	Pro	Pro
	Thr 280	Gly	Gln	Tyr	Thr	Leu 285	Phe	Pro	Leu	Pro	Pro 290	Thr	Leu	Pro	Thr
30	Pro 295	Val	Val	Gln	Leu	His 300	Prd	Leu	Leu	Pro	Asp 305	Pro	Ser	Ala	Pro
L .	Thr 310	Pro	Thr	Pro	Thr	Ser 315	Pro	Lau	Leu	Asn	Thr 320	Ser	Tyr	Thr	His
35	Ser 325	Gln	Asn	Leu	Ser	Gln 330	Glu	Gly 332							
	(2)	INFO	RMAT	ON I	FOR S	SEQ]	D NO	0:2:	/	\					
40	(:	(1	EQUENA) LI B) TY C) ST	ENGTI (PE : [RANI	H: 17 nucl DEDNE	795 k Leic ESS:	ases acio sino	i i			\				
45	(x:	i) SI	EQUE	NCE I	DESCI	RIPTI	ON:	SEQ	ID 1	10:2	: \	\			
	TCT"	TCCT	ACC (CATCI	rgcto	CC CC	CAGAC	GGC1	r GCC	CTGCT	TGTG	CACT	rtggc	GTC 5	50
50	CTG	GAGC	CCT I	CTC	CACC	CG GI	ATAGA	ATTCO	C TCA	ACCCI	TGG	ccc	CTI	TTG 1	L00

CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150 GACACCCCOG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350 AGACTGAGCC AGTGCCCAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500 ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550 GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CXACAGCTCA CAAGGATCCC 650 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700 CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGÒGG GCCCCACCCA 750 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800 CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCAAGA 900 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGQA 950 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTTCC

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TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050 CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100 5 CCAACCGATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150 10 CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250 15 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300 20 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350 AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400 GGGATACACA GGACTGAAAA GGGAATCATT TTTCACTGTA CATTATAAAC 1450 CTTCAGAAGC TATTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500 GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550 35 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600 GAACAGAGG AGAGACTAAC CTTGAGTCAG ÀAAACAGAGA AAGGGTAATT 1650 40 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700 CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750 45

(2) INFORMATION FOR SEQ ID NO:3:

	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
	Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu -16 -15 -5
10	Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys 1 5 10
15	Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu 15 20 25 26
	(2) INFORMATION FOR SEQ ID NO:4:
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 390 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
	GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
30	CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100
⊁ ∖ 35	GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT 150
	CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA 200
40	GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA 250
	CTCCCAGGAA GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT 300
45	TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT 350
	TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

	(2) \INFORMATION FOR SEQ ID NO:5:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 390 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
	CTTAAGGACC TATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA	50
15	GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA	100
	CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA	150
20	GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT	200
25	CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT	250
3 pt	GAGGGTCCTT CTGTGGTAGT GAGGAGATT GAGGAACTGG GTTACTGATA	300
30	AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA	350
L .	AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT 390	
35	(2) INFORMATION FOR SEQ ID NO:6:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 332 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	
	Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys	Leu 15
50	Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys	s Pro

	ŒŲu	Val	His	Pro	Leu 35	Pro	Thr	Pro	Val	Leu 40	Leu	Pro	Ala	Val	Asp 45
5	Phe	Ser	Leu	Gly	Glu 50	Trp	Lys	Thr	Gln	Met 55	Glu	Glu	Thr	Lys	Ala 60
	Gln	Asp	le	Leu	Gly 65	Ala	Val	Thr	Leu	Leu 70	Leu	Glu	Gly	Val	Met 75
10	Ala	Ala	Arg	Gly	Gln 80	Leu	Gly	Pro	Thr	Cys 85	Leu	Ser	Ser	Leu	Leu 90
15	Gly	Gln	Leu	Ser	Gly \95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
13	Ser	Leu	Leu	Gly	Thr 110	Gln	Leu	Pro	Pro	Gln 115	Gly	Arg	Thr	Thr	Ala 120
20	His	Lys	Asp	Pro	Asn 125	Ala	Ile	Phe	Leu	Ser 130	Phe	Gln	His	Leu	Leu 135
	Arg	Gly	Lys	Val	Arg 140	Phe	Деи	Met	Leu	Val 145	Gly	Gly	Ser	Thr	Leu 150
	Cys	Val	Arg	Arg	Ala 155	Pro	Pro	Thr	Thr	Ala 160	Val	Pro	Ser	Arg	Thr 165
30	Ser	Leu	Val	Leu	Thr 170	Leu	Asn	Glu	Leu	Pro 175	Asn	Arg	Thr	Ser	Gly 180
L .	Leu	Leu	Glu	Thr	Asn 185	Phe	Thr	Ala	Ser	Ala 190	Arg	Thr	Thr	Gly	Ser 195
35	Gly	Leu	Leu	Lys	Trp 200	Gln	Gln	Gly	Phe	Arg 205	Ala	Lys	Ile	Pro	Gly 210
	Leu	Leu	Asn	Gln	Thr 215	Ser	Arg	Ser	Leu	Asp 220	Gln	Ile	Pro	Gly	Tyr 225
40	Leu	Asn	Arg	Ile	His 230	Glu	Leu	Leu	Asn	Gly 235	Thr	Arg	Gly	Leu	Phe 240
45	Pro	Gly	Pro	Ser	Arg 245	Arg	Thr	Leu	Gly	Ala 250	Pro	Asp	\le	Ser	Ser 255
43	Gly	Thr	Ser	Asp	Thr 260	Gly	Ser	Leu	Pro	Pro 265	Asn	Leu	Gln	Pro	Gly 270
50	Tyr	Ser	Pro	Ser	Pro 275	Thr	His	Pro	Pro	Thr 280	Gly	Gln	Tyr	Thr	Leu \2 85

	Rhe	Pro	Leu	Pro	Pro 290	Thr	Leu	Pro	Thr	Pro 295	Val	Val	Gln	Leu	His 300
5	Pro	Leu	Leu	Pro	Asp 305	Pro	Ser	Ala	Pro	Thr 310	Pro	Thr	Pro	Thr	Ser 315
	Pro	Leu	Leu	Asn	Thr 320	Ser	Tyr	Thr	His	Ser 325	Gln	Asn	Leu	Ser	Gln 330
10	Glu	Gly 332													
	(2)	INFO	RMAT:	гои/і	FOR S	SEQ :	ID NO	0:7:							
15	(:	(<u>)</u>	A) L1 B) T		1: 10 ami	66 ar 20 ac			is						
20	(x:	i) SI	EQUEI	NCE I	DESCI	RIP T	ION:	SEQ	ID 1	10:7	:				
	Ala 1	Pro	Pro	Arg	Leu 5	Ile	gha	Asp	Ser	Arg 10	Val	Leu	Glu	Arg	Tyr 15
25	Leu	Leu	Glu	Ala	Lys 20	Glu	Ala	Glu	Asn	Ile 25	Thr	Thr	Gly	Cys	Ala 30
CONT.	Glu	His	Cys	Ser	Leu 35	Asn	Glu	Asn	Ile	Thr 40	Val	Pro	Asp	Thr	Lys 45
,	Val	Asn	Phe	Tyr	Ala 50	Trp	Lys	Arg	Met	Glu 55	Val	Gly	Gln	Gln	Ala 60
⊁ ∙ 35	Val	Glu	Val	Trp	Gln 65	Gly	Leu	Ala	Leu	Leu 70	Ser	Glu	Ala	Val	Leu 75
	Arg	Gly	Gln	Ala	Leu 80	Leu	Val	Asn	Ser	Ser 85	Gln	Pro	Trp	Glu	Pro 90
40	Leu	Gln	Leu	His	Val 95	Asp	Lys	Ala	Val	Ser 100	Gly	Leu	Arg	Ser	Leu 105
<i>1</i> E	Thr	Thr	Leu	Leu	Arg 110	Ala	Leu	Gly	Ala	Gln 115	Lys	Glu	Ala	Ile	Ser 120
45	Pro	Pro	Asp	Ala	Ala 125	Ser	Ala	Ala	Pro	Leu 130	Arg	Thr	ΙÌę	Thr	Ala 135
50	Asp	Thr	Phe	Arg	Lys 140	Leu	Phe	Arg	Val	Tyr 145	Ser	Asn	Phe	Leu	Arg 150

	Gly	Lys	Leu	Lys	Leu 155	Tyr	Thr	Gly	Glu	Ala 160	Cys	Arg	Thr	Gly	Asr 165
5	Arg														
	(2)	гиђо	RMAT:	ION I	FOR S	SEQ :	ID NO	0:8:							
10	(:	(1	B) Æ.	ENGTI YPE :	CHARA H: 32 amin DGY:	28 ar	mino cid		ds						
15	(x:	i) S	EQUEI	NCE I	DESCI	RIPT	ION:	SEQ	ID I	10:8	:				
15	Ser 1	Pro	Ala	Pro	Pro 5	Ala	Cys	Asp	Leu	Arg 10	Val	Leu	Ser	Lys	Leu 15
20	Leu	Arg	Asp	Ser	His 20	Val	Leu	His	Ser	Arg 25	Leu	Ser	Gln	Cys	Pro 30
	Glu	Val	His	Pro	Leu 35	Pro	Thr	Pro	Val	Leu 40	Leu	Pro	Ala	Val	Asp 45
35	Phe	Ser	Leu	Gly	Glu 50	Trp	pha	Thr	Gln	Met 55	Glu	Glu	Thr	Lys	Ala
and a	Gln	Asp	Ile	Leu	Gly 65	Ala	Val	Thr	Leu	Leu 70	Leu	Glu	Gly	Val	Met 75
↓.	Ala	Ala	Arg	Gly	Gln 80	Leu	Gly	Pro	Thr	Cys 85	Leu	Ser	Ser	Leu	Leu 90
3 5	Gly	Gln	Leu	Ser	Gly 95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Glr 105
	Ser	Leu	Leu	Gly	Thr 110	Gln	Gly	Arg	Thr	Thr 115	Ala	His	Lys	Asp	Pro 120
40	Asn	Ala	Ile	Phe	Leu 125	Ser	Phe	Gln	His	Leu 130	Leu	Arg	Gly	Lys	Val
45	Arg	Phe	Leu	Met	Leu 140	Val	Gly	Gly	Ser	Thr 145	Leu	Cys \	Val	Arg	Arg 150
15	Ala	Pro	Pro	Thr	Thr 155	Ala	Val	Pro	Ser	Arg 160	Thr	Ser	Leu	Val	Leu 165
50	Thr	Leu	Asn	Glu	Leu 170	Pro	Asn	Arg	Thr	Ser 175	Gly	Leu	Leu	Glu	Thr

	Asn	Phe	Thr	Ala	Ser 185	Ala	Arg	Thr	Thr	Gly 190	Ser	Gly	Leu	Leu	Lys 195
5	Trp	Gln	Gln	Gly	Phe 200	Arg	Ala	Lys	Ile	Pro 205	Gly	Leu	Leu	Asn	Gln 210
	Thr	Ser	Arg	Ser	Leu 215	Asp	Gln	Ile	Pro	Gly 220	Tyr	Leu	Asn	Arg	Ile 225
10	His	Glu	Leu	Leu	Asn 230	Gly	Thr	Arg	Gly	Leu 235	Phe	Pro	Gly	Pro	Ser 240
1 F	Arg	Arg	Thr	Leu	Gly 245	Ala	Pro	Asp	Ile	Ser 250	Ser	Gly	Thr	Ser	Asp 255
15	Thr	Gly	Ser	Leu	Pro 260	Pro	Asn	Leu	Gln	Pro 265	Gly	Tyr	Ser	Pro	Ser 270
20	Pro	Thr	His	Pro	Pro 275	Thr	Gly	Gln	Tyr	Thr 280	Leu	Phe	Pro	Leu	Pro 285
•	Pro	Thr	Leu	Pro	Thr 290	Pico	Val	Val	Gln	Leu 295	His	Pro	Leu	Leu	Pro 300
J25	Asp	Pro	Ser	Ala	Pro 305	Thr	Pro	Thr	Pro	Thr 310	Ser	Pro	Leu	Leu	Asn 315
the right	Thr	Ser	Tyr	Thr	His 320	Ser	Gln	Asn	Leu	Ser 325	Gln	Glu	Gly 328		
30	(2)	INFO	TAM	ON E	FOR S	SEQ 1	D NO	0:9							
<i>3</i> °	(:					ACTER			de la						
35		(I	3) T	PE:	amir	no ac line	cid	acic	\ \						
	(x :	i) SI	EQUE	ICE I	DESC	RIPT	ON:	SEQ	ID N	10:6	:				
40	Ser 1	Pro	Ala	Pro	Pro 5	Ala	Cys	Asp	Leu	Arg 10	Val	Leu	Ser	Lys	Leu 15
4.5	Leu	Arg	Asp	Ser	His 20	Val	Leu	His	Ser	Arg 25	Leu	Ser	Gln	Cys	Pro 30
45	Glu	Val	His	Pro	Leu 35	Pro	Thr	Pro	Val	Leu 40	Leu	Pro	Ala	Val	Asp 45
50	Phe	Ser	Leu	Gly	Glu 50	Trp	Lys	Thr	Gln	Met 55	Glu	Glu	The	Lys \	Ala 60

	GÌm	Asp	Ile	Leu	Gly 65	Ala	Val	Thr	Leu	Leu 70	Leu	Glu	Gly	Val	Met 75
5	Ala	Ala	Arg	Gly	Gln 80	Leu	Gly	Pro	Thr	Cys 85	Leu	Ser	Ser	Leu	Leu 90
	Gly	Gln	Leu	Ser	Gly 95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
10	Ser	Leu	Leu	Gly	Thr 110	Gln	Leu	Pro	Pro	Gln 115	Gly	Arg	Thr	Thr	Ala 120
16	His	Lys	Asp	Pro	Asn 125	Ala	Ile	Phe	Leu	Ser 130	Phe	Gln	His	Leu	Leu 135
15	Arg	Gly	Lys	Asp	Phe	Trp	Ile	Val	Gly	Asp 145	Lys	Leu	His	Cys	Leu 150
20	Ser	Gln	Asn	Tyr	Tro 155	Leu	Trp	Ala	Ser	Glu 160	Val	Ala	Ala	Gly	Ile 165
	Gln	Ser	Gln	Asp	Ser 170	jab	Ser	Ala	Glu	Pro 175	Asn	Leu	Gln	Val	Pro 180
1/25 1/25	Gly	Pro	Asn	Pro	Arg 185	Ile	Pro	Glu	Gln	Asp 190	Thr	Arg	Thr	Leu	Glu 195
S. Mar	Trp	Asn	Ser	Trp	Thr 200	Leu	ser	Trp	Thr	Leu 205	Thr	Gln	Asp	Pro	Arg 210
30	Ser	Pro	Gly	His	Phe 215	Leu	Arg	Asn	Ile	Arg 220	His	Arg	Leu	Pro	Ala 225
35	Thr	Gln	Pro	Pro	Ala 230	Trp	Ile	Phe	Ser	Phe 235	Pro	Asn	Pro	Ser	Ser 240
	Tyr	Trp	Thr	Val	Tyr 245	Ala	Leu	Pro	Ser	Ser 250	Thr	His	Leu	Ala	His 255
40	Pro	Cys	Gly	Pro	Ala 260	Pro	Pro	Pro	Ala	Ser 265					
	(2)	INFOR	TAMS	ON E	OR S	SEQ 1	D NO	0:10:	:						
45	(±	(I	A) LE 3) TY	NCE (ENGTH (PE: OPOL(H: 26 amir	on ac	nino cid		ls	`					
50	(xi	i) SE	EQUE	ICE I	DESCR	RIPT	ON:	SEQ	ID N	10:10):	/			

	Ser	Pro	Ala	Pro	Pro 5	Ala	Cys	Asp	Leu	Arg 10	Val	Leu	Ser	Lys	Leu 15
5	Leu	Arg	Asp	Ser	His 20	Val	Leu	His	Ser	Arg 25	Leu	Ser	Gln	Cys	Pro 30
	Glu	Val	His	Pro	Leu 35	Pro	Thr	Pro	Val	Leu 40	Leu	Pro	Ala	Val	Asp 45
10	Phe	Ser	Leu	Gly	Glu 50	Trp	Lys	Thr	Gln	Met 55	Glu	Glu	Thr	Lys	Ala 60
15	Gln	Asp	Ile	Leb	Gly \65	Ala	Val	Thr	Leu	Leu 70	Leu	Glu	Gly	Val	Met 75
13	Ala	Ala	Arg	Gly	GAn 80	Leu	Gly	Pro	Thr	Cys 85	Leu	Ser	Ser	Leu	Leu 90
20	Gly	Gln	Leu	Ser	Gly 95	dln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
	Ser	Leu	Leu	Gly	Thr 110	Gln	Gly	Arg	Thr	Thr 115	Ala	His	Lys	Asp	Pro 120
1335	Asn	Ala	Ile	Phe	Leu 125	Ser	Phe	Gln	His	Leu 130	Leu	Arg	Gly	Lys	Asp 135
Cont	Phe	Trp	Ile	Val	Gly 140	Asp	Lys	Leu	His	Cys 145	Leu	Ser	Gln	Asn	Tyr 150
	Trp	Leu	Trp	Ala	Ser 155	Glu	Val	Ala	Ala	Gly 160	Ile	Gln	Ser	Gln	Asp 165
35	Ser	Trp	Ser	Ala	Glu 170	Pro	Asn	Leu	Gln	Val 175	Pro	Gly	Pro	Asn	Pro 180
	Arg	Ile	Pro	Glu	Gln 185	Asp	Thr	Arg	Thr	Leu 190	Glu	Trp	Asn	Ser	Trp 195
40	Thr	Leu	Ser	Trp	Thr 200	Leu	Thr	Gln	Asp	Pro 205	Arg	Ser	Pro	Gly	His 210
45	Phe	Leu	Arg	Asn	Ile 215	Arg	His	Arg	Leu	Pro 220	Ala	thr	Gln	Pro	Pro 225
10	Ala	Trp	Ile	Phe	Ser 230	Phe	Pro	Asn	Pro	Ser 235	Ser	Tyr	Trp	Thr	Val 240
50	Tyr	Ala	Leu	Pro	Ser 245	Ser	Thr	His	Leu	Ala 250	His	Pro	Cya	Gly	Pro 255

Ala Pro Pro Pro Ala Ser 260 261

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1443 bases
 - (B) TYPE: nucleic acid
 - (C)\STRANDEDNESS: single
 - (D) YOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGTCCTTGG CCCACCTCT TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50 AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100 ATACAGGGAG CCACTTCAGT\TAGACACCCT GGCCAGAATG GAGCTGACTG 150 ATTTGCTCCT GGCGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC 200 AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG 250 TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300 CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG YGGACTTTAG CCTGGGAGAA 350 TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400 GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450 CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500 TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA 550 CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACTG CTTCGGGGAA 600 AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTCAGACGG 650

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ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT 700 AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG 750 5 TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC 800 AGAGTCAAGA\TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT 850 10 CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAACTC 900 15 ATGGGCTCTT TGCTG&AACC TCACTTCAGA CCCTGGAAGC CTCAGACATC 950 TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG 1000 20 ACTTCCTCCT TCTCCAAGCC TGCTCCTGA TGGACACACA CCCTTCCCTC 1050 CTTCACCTGC CTTGCCCACC ACCATGGAT CTCCACCCCA GCTCCACCCC 1100 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC 1150 AGTCACAATG TACCCTCATC CCAGGAATT GTCTCAGGAA ACATAGCGCG 1200 GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC 1250 AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT 1300 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATGT AAAATTTTAG 1350 40 GAGCTATTTT TTTTTAACCT ATCAGCAATA TTCATCAGAG CAGCTAGCGA 1400 45 TCTTTGGTCT ATTTTCGGTA TAAATTTGAA AATCACTAAT TOT 1443

(2) INFORMATION FOR SEQ ID NO:12:

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(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid (D) TOPOLOGY: linear 5 SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val -21 -20 -15 10 Ala Arg Leù Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Agn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser 10 15 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val\Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln 20 Thr Glu Gln Ser Lys Alà Gln Asp Ile Leu Gly Ala Val Ser Leu 55 Leu Leu Glu Gly Val Met Ala Arg Gly Gln Leu Glu Pro Ser 70 75 Cys Leu Ser Ser Leu Leu Gly 🗘 In Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Gly Leu\Leu Gly Thr Gln Gly Arg Thr 100 110 Thr Ala His Lys Asp Pro Asn Ala Le\ Phe Leu Ser Leu Gln Gln 115 35 120 125 Leu Leu Arg Gly Lys Val Arg Phe Leu Deu Leu Val Glu Gly Pro 130 135 140 Thr Ala Val Pro Ser 40 Thr Leu Cys Val Arg Arg Thr Leu Pro Thr 150 Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr 160 45 Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala 175 180 185 Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe Arg **V**al Lys Ile 50 190 195 200

(A) LENGTH: 352 amino acids

	Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile 205 210 215
5	Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His 220 230
	Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp 235 240 245
10	Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu 250 255 260
15	Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro Asp Gly His 265 270 275
13	Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr His Gly Ser 280 290
20	Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr Met 300 305
	Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro 310 320
125 X	Arg Asn Leu Ser Gln Glu Thr 325 330 331
CALA	(2) INFORMATION FOR SEQ ID NO: 13:
**************************************	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1536 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
40	GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50
	AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100
45	ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150
50	ATTTGCTCCT GGCGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC 200
50	AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG 250

TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300 CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350 5 TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400 GTCCCTTCTA\CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450 10 CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500 15 TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGCTTCCTC TACAGGGCAG 550 GACCACAGCT CACAAGGACC CCAATGCCCT CTTCTTGAGC TTGCAACAAC 600 20 TGCTTCGGGG AAAGGTGCGC TYCCTGCTTC TGGTAGAAGG TCCCACCCTC 650 TGTGTCAGAC GGACCCTGCC AACCACAGCT GTCCCAAGCA GTACTTCTCA 700 ACTCCTCACA CTAAACAGT TCCCAAACAG GACTTCTGGA TTGTTGGAGA 750 CGAACTTCAG TGTCACAGCC AGAACTGCTG OCCCTGGACT TCTGAGCAGG 800 CTTCAGGGAT TCAGAGTCAA GATTACTCCT GGTCAGCTAA ATCAAACCTC 850 CAGGTCCCCA GTCCAAATCT CTGGATACCT GAACAGGACA CACGGACCTG 900 TGAATGGAAC TCATGGGCTC TTTGCTGGAA CCTCACTTCA\GACCCTGGAA 950 40 GCCTCAGACA TCTCGCCCGG AGCTTTCAAC AAAGGCTCCC TGGCATTCAA 1000 45 CCTCCAGGGT GGACTTCCTC CTTCTCCAAG CCTTGCTCCT GATGGAXACA 1050 CACCCTTCCC TCCTTCACCT GCCTTGCCCA CCACCCATGG ATCTCCACC 1100 50 CAGCTCCACC CCCTGTTTCC TGACCCTTCC ACCACCATGC CTAACTCTAC 11/50

	COCCCTCAT	CCAGTCACAA	TGTACCCTCA	TCCCAGGAAT	TTGTCTCAGG	1200
5	AAACATAGCG	CGGGCACTGG	CCCAGTGAGC	GTCTGCAGCT	TCTCTCGGGG	1250
	ACAAGCTTCC	CCAGGAAGGC	TGAGAGGCAG	CTGCATCTGC	TCCAGATGTT	1300
10	CTGCTTTCAC	CTAAAAGGCC	CTGGGGAAGG	GATACACAGC	ACTGGAGATT	1350
15	GTAAAATTTT	AGGAGCTATT	TTTTTTTAAC	CTATCAGCAA	TATTCATCAG	1400
	AGCAGCTAGC	GATCTTTGGT	CTATTTTCGG	TATAAATTTG	AAAATCACTA	1450
20	АААААААА	АААААААА	АААААААА	АААААААА	АААААААА	1500
	ААААААААА	АААААААА	ааааааа	AAAAAA 1536	5	

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) INFORMATION FOR SEQ ID NO 14:

(i) SEQUENCE CHARACTERISTICS?

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val -21 -20 -15 -10

Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
-5

Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser 10 15 20

Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Lle Pro Val
25 30 35

Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln 40 45 50

Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu 55 60 65

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu\Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Ala Val Pro Ser Ser Pro Asn Arg Thr Ser Gly\Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gl \text{\chi} Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly G λ n Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Sex Pro Ser Leu Ala Pro Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His Gly Ser Pro Pro Gln Leu His Pro Leu Phe Rro Asp Pro Ser Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met

	325	Pro	HIS	Pro	Arg	330	Leu	ser	GIN	GIU	335				
	(2)	иго	RMAT	ION 1	FOR S	SEQ :	ID N	0:15	:						
5	(:	· \	A) Li	ENGTI YPE :	CHARA H: 24	41 ar	mino cid		ds						
10	(x :	•			OGY: DESCI			SEQ	ID 1	NO:15	5:				
1.5	Ser 1	Pro	Val	Ala	Pro 5	Ala	Cys	Asp	Pro	Arg 10	Leu	Leu	Asn	Lys	Leu 15
15	Leu	Arg	Asp	Ser	His 20	Leu	Leu	His	Ser	Arg 25	Leu	Ser	Gln	Cys	Pro 30
20	Asp	Val	Asp	Pro	Leu 35	Ser	Ile	Pro	Val	Leu 40	Leu	Pro	Ala	Val	Asp 45
	Phe	Ser	Leu	Gly	Glu 50	Trp	Lys	Thr	Gln	Thr 55	Glu	Gln	Ser	Lys	Ala 60
25	Gln	Asp	Ile	Leu	Gly 65	Ala	Val	Ser	Leu	Leu 70	Leu	Glu	Gly	Val	Met 75
30	Ala	Ala	Arg	Gly	Gln 80	Leu	Glu	Pro	Ser	Cys 85	Leu	Ser	Ser	Leu	Leu 90
	Gly	Gln	Leu	Ser	Gly 95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
35	Gly	Leu	Leu	Gly	Thr 110	Gln	Leu	Pro	Leu	Gln 115	Gly	Arg	Thr	Thr	Ala 120
l out	His	Lys	Asp	Pro	Asn 125	Ala	Leu	Phe	Leu	Sex 130		Gln	Gln	Leu	Leu 135
48	Arg	Gly	Lys	Asp	Phe 140	Trp	Ile	Val	Gly	Asp 145	GJų	Leu	Gln	Cys	His 150
45	Ser	Gln	Asn	Cys	Trp 155	Pro	Trp	Thr	Ser	Glu 160	Gln	Ala	Ser	Gly	Ile 165
	Gln	Ser	Gln	Asp	Tyr 170	Ser	Trp	Ser	Ala	Lys 175	Ser	Asn	Leu	Gln	Val 180
50	Pro	Ser	Pro	Asn	Leu 185	Trp	Ile	Pro	Glu	Gln 190	Asp	Thr	Arg	Thr	Cys 195

	`												
	dlu Trp A	sn Ser	Trp 200	Ala	Leu	Cys	Trp	Asn 205	Leu	Thr	Ser	Asp	Pro 210
5	Gly Ser L	eu Arg	His 215	Leu	Ala	Arg	Ser	Phe 220	Gln	Gln	Arg	Leu	Pro 225
	Gly Ile G	ln Pro	Pro 230	Gly	Trp	Thr	Ser	Ser 235	Phe	Ser	Lys	Pro	Cys 240
10	Ser 241												
	(2) INFORM	/NOITA	FOR S	EQ I	D NO):16:	:						
15			1:\33 amin	5 am	nino cid		ls						
20	(xi) SEQ	UENCE I	DESCR	1941	ON:	SEQ	ID N	NO:16	5:				
	Ser Pro V	al Ala	Pro 5	Ala	cha	Asp	Pro	Arg 10	Leu	Leu	Asn	Lys	Leu 15
25	Leu Arg A	sp Ser	His 20	Leu	Leu	His	Ser	Arg 25	Leu	Ser	Gln	Cys	Pro 30
30	Asp Val A	sp Pro	Leu 35	Ser	Ile	Pro	Val	Leu 40	Leu	Pro	Ala	Val	Asp 45
∤ ·	Phe Ser L	eu Gly	Glu 50	Trp	Lys	Thr	Glb	Thr	Glu	Gln	Ser	Lys	Ala 60
35	Gln Asp I	le Leu	Gly 65	Ala	Val	Ser	Leu	Leu 70	Leu	Glu	Gly	Val	Met 75
$\langle \chi \rangle$	Ala Ala A	rg Gly	Gln 80	Leu	Glu	Pro	Ser	Cys 85	Leu	Ser	Ser	Leu	Leu 90
	Gly Gln L	eu Ser	Gly 95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
45	Gly Leu L	eu Gly	Thr 110	Gln	Leu	Pro	Leu	Gln 115	Gly	Arg	Thr	Thr	Ala 120
ŦJ	His Lys A	sp Pro	Asn 125	Ala	Leu	Phe	Leu	Ser 130	Leu	Gln	GÌn	Leu	Leu 135
50	Arg Gly L	ys Val	Arg 140	Phe	Leu	Leu	Leu	Val 145	Glu	Gly	Pro	Thr	Leu 150

	ç y s	Val	Arg	Arg	Thr 155	Leu	Pro	Thr	Thr	Ala 160	Val	Pro	Ser	Ser	Thr 165
5	Ser	Gln	Leu	Leu	Thr 170	Leu	Asn	Lys	Phe	Pro 175	Asn	Arg	Thr	Ser	Gly 180
	Leu	Leu	Glu	Thr	Asn 185	Phe	Ser	Val	Thr	Ala 190	Arg	Thr	Ala	Gly	Pro 195
10	Gly	Leu	Leu	Ser	Arg 200	Leu	Gln	Gly	Phe	Arg 205	Val	Lys	Ile	Thr	Pro 210
1.5	Gly	Gln	Leu	Asn	Gln 215	Thr	Ser	Arg	Ser	Pro 220	Val	Gln	Ile	Ser	Gly 225
15	Tyr	Leu	Asn	Arg	Thr 230	His	Gly	Pro	Val	Asn 235	Gly	Thr	His	Gly	Leu 240
20	Phe	Ala	Gly	Thr	Ser 245	Leu	Gln	Thr	Leu	Glu 250	Ala	Ser	Asp	Ile	Ser 255
	Pro	Gly	Ala	Phe	Asn 260	Lys	Gly	Ser	Leu	Ala 265	Phe	Asn	Leu	Gln	Gly 270
25	Gly	Leu	Pro	Pro	Ser 275	Pro	Ser	Leu	Ala	Pro 280	Asp	Gly	His	Thr	Pro 285
20	Phe	Pro	Pro	Ser	Pro 290	Ala	Leu	Pro	Thr	Thr 295	His	Gly	Ser	Pro	Pro. 300
30 L .	Gln	Leu	His	Pro	Leu 305	Phe	Pro	Asp	Pro	Ser 310	Thr	Thr	Met	Pro	Asn 315
\bar{B} 5	Ser	Thr	Ala	Pro	His 320	Pro	Val	Thr	Met	Tyr 325	Pro	His	Pro	Arg	Asn 330
2, 7 mp, 7	Leu	Ser	Gln	Glu	Thr 335					`					
CARL CONTRACTOR	(2)	INFO	RMATI	ON I	FOR S	SEQ]	D NO	0:17:	:		\				
45	t)	(Z	•	ENGTI (PE :		32 am 10 ac	nino cid		ls						
	(xi	i) SI	EQUE	ICE I	DESCF	RIPTI	ON:	SEQ	ID N	NO:17	7 :		/		
50	Ser 1	Pro	Ala	Pro	Pro 5	Ala	Cys	Asp	Pro	Arg	Leu	Leu	Asn	LXs	Leu 15

		Lèu	Arg	Asp	Ser	His 20	Val	Leu	His	Gly	Arg 25	Leu	Ser	Gln	Cys	Pro 30
5		Asp	Ile	Asn	Pro	Leu 35	Ser	Thr	Pro	Val	Leu 40	Leu	Pro	Ala	Val	Asp 45
		Phe	Thr	Leu	Gly	Glu 50	Trp	Lys	Thr	Gln	Thr 55	Glu	Gln	Thr	Lys	Ala 60
10		Gln	Asp	Val	Deu	Gly 65	Ala	Thr	Thr	Leu	Leu 70	Leu	Glu	Ala	Val	Met 75
1 5		Thr	Ala	Arg	Gly	Gln 80	Val	Gly	Pro	Pro	Cys 85	Leu	Ser	Ser	Leu	Leu 90
15		Val	Gln	Leu	Ser	Gly 95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
20		Asp	Leu	Leu	Gly	Met 110	Gln	Leu	Pro	Pro	Gln 115	Gly	Arg	Thr	Thr	Ala 120
		His	Lys	Asp	Pro	Ser 125	Ala	Ile	Phe	Leu	Asn 130	Phe	Gln	Gln	Leu	Leu 135
25		Arg	Gly	Lys	Val	Arg 140	Phe	Leu	Led	Leu	Val 145	Val	Gly	Pro	Ser	Leu 150
30		Cys	Ala	Lys	Arg	Ala 155	Pro	Pro	Ala	Ile	Ala 160	Val	Pro	Ser	Ser	Thr 165
) ₄ .		Ser	Pro	Phe	His	Thr 170	Leu	Asn	Lys	Leu	Pro 175	Asn	Arg	Thr	Ser	Gly 180
J 35	_	Leu	Leu	Glu	Thr	Asn 185	Ser	Ser	Ile	Ser	Ala 190	Arg	Thr	Thr	Gly	Ser 195
B I		Gly	Phe	Leu	Lys	Arg 200	Leu	Gln	Ala	Phe	Arg 205	Ala	Lys	Ile	Pro	Gly 210
410		Leu	Leu	Asn	Gln	Thr 215	Ser	Arg	Ser	Leu	Asp 220	Gln	Ile	Pro	Gly	His 225
45		Gln	Asn	Gly	Thr	His 230	Gly	Pro	Leu	Ser	Gly 235	Ile	His	GAY	Leu	Phe 240
ŦJ		Pro	Gly	Pro	Gln	Pro 245	Gly	Ala	Leu	Gly	Ala 250	Pro	Asp	Ile	Pro	Pro 255
50		Ala	Thr	Ser	Gly	Met 260	Gly	Ser	Arg	Pro	Thr 265	Tyr	Leu	Gln	Pro	Gly 270

	Glu Ser Pro	o Ser	Pro <i>P</i> 275	Ala	His	Pro	Ser	Pro 280	Gly	Arg	Tyr	Thr	Leu 285
5	Phe Ser Pro	o Ser	Pro 7	Thr	Ser	Pro	Ser	Pro 295	Thr	Val	Gln	Leu	Gln 300
	Pro Leu Le	u Pro	Asp I	Pro	Ser	Ala	Ile	Thr 310	Pro	Asn	Ser	Thr	Ser 315
10	Pro Leu Le	u Phe	Ala <i>A</i> 320	Ala	His	Pro	His	Phe 325	Gln	Asn	Leu	Ser	Gln 330
15	Glu Glu 332 (2) INFORMA	rion f	FOR SU	Ξ Q]	ID NO):18:	:						
20	(B) (C)	ENCE (LENGTH LYPE: STRANI LOPOLO	H: 102 nucle DEDNES	26 k eic SS:	ases acid	3 1							
25	(xi) SEQU	ENCE I)ESCR1	[PT]	ION:	SEQ	ID N	10:18	3:				
	ÄGCCCGGCTC	CTCCT	GCCT	J TO	GACCO	CCCGF	CTC	CCTA	ATA	AACT	rgcti	rcg .	50
30	TGACTCCCAT	GTCCI	TCAC	G GC	CAGAC	CTGAG	G CCI	ACTGO	CCCA	GAC	ATTA	ACC :	100
.	CTTTGTCCAC	ACCT	STCCTO	G CI	rgcci	CGCT	G TGC	ACT	rZAC	CTT	GGAG	BAA :	150
35	TGGAAAACCC	AGACG	GAGC	A GA	ACAAA	AGGC	A CAC	GATO	STCC	ÆGG	GAGCC	CAC	200
8 N (4)	AACCCTTCTG	CTGGA	AGGCA	3 T(GATGA	ACAGO	C ACC	GGG <i>I</i>	ACAA	GTG	GACC	CCC :	250
7	CTTGCCTCTC	ATCCC	CTGCTO	G GT	rgcac	CTTI	CTC	GACA	AGGT	TCG	сстф	CTC	300
45	CTCGGGGCCC	TGCAG	GACCI	r co	CTTGG	BAATO	CAC	CTTC	CCTC	CACA	AGGGA	AAG	350
	GACCACAGCT	CACAA	\GGAT(C CC	CAGTO	SCCAT	CTI	CCTC	SAAC	TTC	CAACA	AAC	400
50	TGCTCCGAGG	AAAGG	TGCGT	r T	CCTG	CTCC	TTO	TAGI	GGG	GCC	CTCCC	CTC	450

YGTGCCAAGA GGGCCCCACC CGCCATAGCT GTCCCGAGCA GCACCTCTCC 500 ATTCACACA CTGAACAAGC TCCCAAACAG GACCTCTGGA TTGTTGGAGA 550 5 CAAACT&CAG TATCTCAGCC AGAACTACTG GCTCTGGATT TCTCAAGAGG 600 CTGCAGGCAT TCAGAGCCAA GATTCCTGGT CTGCTGAACC AAACCTCCAG 650 10 GTCCCTAGAC CANATCCCTG GACACCAGAA TGGGACACAC GGACCCTTGA 700 15 GTGGAATTCA TGGACXCTTT CCTGGACCCC AACCCGGGGC CCTCGGAGCT 750 CCAGACATTC CTCCAGCAAC TTCAGGCATG GGCTCCCGGC CAACCTACCT 800 20 CCAGCCTGGA GAGTCTCCTT CCCCAGCTCA CCCTTCTCCT GGACGATACA 850 CTCTCTTCTC TCCTTCACCC ACCTCGCCCT CCCCCACAGT CCAGCTCCAG 900 25 CCTCTGCTTC CTGACCCCTC TGCGATCACA CCCAACTCTA CCAGTCCTCT 950 30 TCTATTTGCA GCTCACCCTC ATTTCCAGAA\CCTGTCTCAG GAAGAGTAAG 1000 GTGCTCAGAC CCTGCCAACT TCAGCA 1026

(2) INFORMATION FOR SEO ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1014 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
- AGCCCGGCTC CTCCTGCCTG TGACCCCCGA CTCCTAAATA AACTGCTTCG 50

 TGACTCCCAT GTCCTTCACG GCAGACTGAG CCAGTGCCCA GACATTAACC 100

CTTTGTCCAC ACCTGTCCTG CTGCCTGCTG TGGACTTCAC CTTGGGAGAA 150 TGGAAACCC AGACGGAGCA GACAAAGGCA CAGGATGTCC TGGGAGCCAC 200 AACCCTTCTG CTGGAGGCAG TGATGACAGC ACGGGGACAA GTGGGACCCC 250 CTTGCCTCTC AXCCCTGCTG GTGCAGCTTT CTGGACAGGT TCGCCTCCTC 300 CTCGGGGCCC TGCAGGACCT CCTTGGAATG CAGGGAAGGA CCACAGCTCA 350 CAAGGATCCC AGTGCCATOT TCCTGAACTT CCAACAACTG CTCCGAGGAA 400 AGGTGCGTTT CCTGCTCCTT GYAGTGGGGC CCTCCCTCTG TGCCAAGAGG 450 GCCCCACCCG CCATAGCTGT CCCGAGCAGC ACCTCTCCAT TCCACACACT 500 GAACAAGCTC CCAAACAGGA CCTCTGGATT GTTGGAGACA AACTCCAGTA 550 TCTCAGCCAG AACTACTGGC TCTGGATTTC CAAGAGGCT GCAGGCATTC 600 AGAGCCAAGA TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTAGACCA 650 AATCCCTGGA CACCAGAATG GGACACACGG ACCCTTGAGT GGAATTCATG 700 GACTCTTTCC TGGACCCCAA CCCGGGGCCC TCGGAGCTCC AGACATTCCT 750 CCAGCAACTT CAGGCATGGG CTCCCGGCCA ACCTACCTCC AGCCTGGAGA 800 GTCTCCTTCC CCAGCTCACC CTTCTCCTGG ACGATACACT CTCTTCTCTC 850 CTTCACCCAC CTCGCCCTCC CCCACAGTCC AGCTCCAGCC TCTGCTTCCT 900 GACCCCTCTG CGATCACACC CAACTCTACC AGTCCTCTTC TATTTGCAGC 950

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5	TGC	SAAC"	TTC A	AGCA	1014	1									
	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:20	:						
10	(:	(<u>)</u> (<u>)</u>	A) LI 3) T	ENGTI PE:	H: 32 amir				ls						
15	(x:	i) SI	EQUE	ICE I	DESC	RIPT	ON:	SEQ	ID N	10:20):				
	Ser 1	Pro	Ala	Pro	Pro 5	Ala	Cys	Asp	Pro	Arg 10	Leu	Leu	Asn	Lys	Leu 15
20	Leu	Arg	Asp	Ser	His 20	Val	Leu	His	Gly	Arg 25	Leu	Ser	Gln	Cys	Pro 30
25	Asp	Ile	Asn	Pro	Leu 35	Ser	Thr	Pro	Val	Leu 40	Leu	Pro	Ala	Val	Asp 45
23	Phe	Thr	Leu	Gly	Glu 50	Trp	Lys	Thr	Gln	Thr 55	Glu	Gln	Thr	Lys	Ala 60
30	Gln	Asp	Val	Leu	Gly 65	Ala	Thr	Thr	Leu	Leu 70	Leu	Glu	Ala	Val	Met 75
t.	Thr	Ala	Arg	Gly	Gln 80	Val	Gly	Pro	Pro	Cys 85	Leu	Ser	Ser	Leu	Leu 90
35	Val	Gln	Leu	Ser	Gly 95	Gln	Val	Arg	Leu	Leu 100	Leu	Gly	Ala	Leu	Gln 105
	Asp	Leu	Leu	Gly	Met 110	Gln	Gly	Arg	Thr	Thr 115	Ala	His	Lys	Asp	Pro 120
Nº Y	Ser	Ala	Ile	Phe	Leu 125	Asn	Phe	Gln	Gln	Leu 130	Leu	Arg	Gly	Lys	Val 135
45	Arg	Phe	Leu	Leu	Leu 140	Val	Val	Gly	Pro	Ser 145	Leu	Cys	Ala	Lys	Arg 150
	Ala	Pro	Pro	Ala	Ile 155	Ala	Val	Pro	Ser	Ser 160	Thr	Ser	Pro	Phe	His 165
50	Thr	Leu	Asn	Lys	Leu 170	Pro	Asn	Arg	Thr	Ser 175	Gly	Leu	Leu	Glù	Thr 180

TCACCCTCAT TTCCAGAACC TGTCTCAGGA AGAGTAAGGT GCTCAGACCC 1000

	Asn Ser Ser Ile Ser Ala Arg Thr Thr Gly Ser Gly Phe Leu Lys 185 190 195	
5	Arg Leu Gln Ala Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln 200 205 210	
	Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly His Gln Asn Gly Thr 215 220 225	
10	His Gly Pro Leu Ser Gly Ile His Gly Leu Phe Pro Gly Pro Gln 230 235 240	
15	Pro Gly Ala Pro Asp Ile Pro Pro Ala Thr Ser Gly 245 250 255	
15	Met Gly Ser Arg Pro Thr Tyr Leu Gln Pro Gly Glu Ser Pro Ser 260 265 270	
20	Pro Ala His Pro Ser Pro Gly Arg Tyr Thr Leu Phe Ser Pro Ser 275 280 285	
	Pro Thr Ser Pro Ser Pro Thr Val Gln Leu Gln Pro Leu Leu Pro 290 295 300	
25	Asp Pro Ser Ala Ile Thr Pro Asn Ser Thr Ser Pro Leu Leu Phe 305 310 315	
30	Ala Ala His Pro His Phe Gla Asn Leu Ser Gln Glu Glu 320 325 328	
30 !	(2) INFORMATION FOR SEQ ID NO 21:	
*	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 amino acids	
35	(B) TYPE: amino acid (D) TOPOLOGY: linear	
W +	(xi) SEQUENCE DESCRIPTION: SEQ IN NO:21:	
A DO	Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu 1 5 15	
1	Leu Arg Asp Asp His Val Leu His Gly Arg	
45	(2) INFORMATION FOR SEQ ID NO:22:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	

	(x) SEQUENCE DESCRIPTION: SEQ ID NO:22:
F	Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu 1 5 10 15
5	Leu Arg Asp Asp His Ser Val Leu His Gly Arg Leu 20 25 27
10	(2) INFORMATION FOR SEQ ID NO:23:
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
20	Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu 1 10 15
	Leu Arg Asp Asp His Val Leu His Gly Arg 20 25
25	(2) INFORMATION FOR SEQ ID NO:24:
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
ما ا	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
cont,	Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys 1 5 10 14
lub	(2) INFORMATION FOR SEQ ID NO:25:
Popul	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ TO NO:25:
45	Pro Arg Leu Leu Asn Lys Leu Leu Arg 1 5
	(2) INFORMATION FOR SEQ ID NO:26:
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 bases (B) TYPE: nucleic acid

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
	GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45
10	(2) INFORMATION FOR SEQ ID NO:27:
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
	CCNGCNCCNC CNGCNTOYGA 20
25	(2) INFORMATION FOR SEQ ID NO:28:
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
⊬ 35	(xi) SEQUENCE DESCRIPTION SEQ ID NO:28:
	NCCRTGNARN ACRTGRTCRT C 21
	(2) INFORMATION FOR SEQ ID NO:29
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
	CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

	TGACCACGTT CAGCACGGC 69
5	(2) INFORMATION FOR SEQ ID NO:30:
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
	GCCGTGCTGA ACGTGGTCAT CACGAGGCAG TTTATTTAGG AGTCGGGGGT 50
20	CACAGGCTGG CGCTGG 69
25	(2) INFORMATION FOR SEQ ID NO:31:
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
y .	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
35 (CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
200	CGACCACGTC CATCACGGC 69
	(2) INFORMATION FOR SEQ ID NO:32:
4 5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
50	(xi) SEQUENCE DESCRIPTION: SEQ TO NO:32:

GCGTGATGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50 CACATGCCGG AGGTGCTGG 69 5 (2) INFORMATION FOR SEQ ID NO:33: (i) SEQUENCE CHARACTERISTICS: 10 (A) LENGTH: 69 bases (B)\TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: CCAGCACCGC CGGQATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50 20 CGATCATGTC TATCAOGGT 69 (2) INFORMATION FOR SEQ ID NO:34: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 69 bases (B) TYPE: nucleià acid (C) STRANDEDNESS:\single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: 35 ACCGTGATAG ACATGATCGT CACGAAGCAG TTTATTTAGG AGTCGGGGGT 50 40 CACATGCCGG CGGTGCTGG 69 (2) INFORMATION FOR SEQ ID NO:35: 45 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single 50 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEO ID NO:35: -136-

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37 5 (2) INFORMATION FOR SEQ ID NO:36: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 bases (A) TYPE: nucleic acid 10 STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36: 15 CAGTCTGCCG TGAAGGACAT GG 22 20 (2) INFORMATION FOR SEQ ID NO:37: (i) SEQUENCE\CHARACTERISTICS: (A) LENGTH: 24 bases (B) TYPE: \nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: TGTGGACTTT AGCTTGGGAG AATG 24 35 (2) INFORMATION FOR SEQ ID NO:38: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 bases (B) TYPE: nucleic \acid 40 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION; SEQ ID NO:38: 45 GGTCCAGGGA CCTGGAGGTT TG 22 50 (2) INFORMATION FOR SEQ ID NO:3\9:

5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
10	ATCGATATCC ATAGCCAGAC ACCCCGGCCA G 31
	(2) INFORMATION FOR SEQ ID NO:40:
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 bases (B) TYPE: nucleic acid
20	(C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
25	GCTAGCTCTA GACAGGAAG GGAGCTGTAC ATGAGA 36
なれ	
320	(2) INFORMATION FOR SEQ ID NO:41:
y .	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 bases (B) TYPE: nucleic acid (C) STRANDEDNESS single
35	(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
40	CTCCTTGGAA CCCAGGGCAG GACC 24
45	(2) INFORMATION FOR SEQ ID NO:42:
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single
50	(D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
	1301

	GGTCCTGCCC TGGGTTCCAA GGAG 24
-	
5	(2) INFORMATION FOR SEQ ID NO:43:
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
	CTGCTCCGAG CAAAGGACTT CTGGATT 27
20	(2) INFORMATION FOR SEQ ID NO:44:
\$5 V	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
Pour	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
.*·	AATCCAGAAG TCCTTTCCTC GGAGCAG 27
35	(2) INFORMATION FOR SEQ ID NO:45:
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
	CCCTCTGCGT CGCGGCGGCC CCACCCAC 28
50	(2) INFORMATION FOR SEQ ID NO:46:

5	(A) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
10	GTGGGTGGGG CCGCCGCGAC GCAGAGGG 28
15	(2) INFORMATION FOR SEQ ID NO:47:
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
25	GACTCGAGGA TCCATCGATT TTTTTTTTTT TTTTT 35
My x	>
Trong .	(2) INFORMATION FOR SEQ ID NO:48:
35 35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
33	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
	(III) SIZSINGI BIBCKII IION, DIQ ID NO.40.
40	GACTCGAGGA TCCATCG 17
45	(2) INFORMATION FOR SEQ ID NO:49:
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 bases (B) TYPE: nucleic acid
50	<pre>(C) STRANDEDNESS: single (D) TOPOLOGY: linear</pre>
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
	-140-

GOTAGCTCTA GAAGCCCGGC TCCTCCTGCC TG 32 5 (2) INFORMATION FOR SEQ ID NO:50: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 bases (A) TYPE: nucleic acid 10 STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEO ID NO:50: 15 CGAAATTAAC CCTCACTAAA G 21 (2) INFORMATION\FOR SEQ ID NO:51: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH\ 4 amino acids (B) TYPE: amino acid (D) TOPOLOGX: linear (xi) SEQUENCE DESORIPTION: SEQ ID NO:51: His Val Leu His 1 (2) INFORMATION FOR SEQ ID NO:52: (i) SEQUENCE CHARACTERISTICS: 35 (A) LENGTH: 4 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 40 (xi) SEQUENCE DESCRIPTION SEQ ID NO:52: Ser Arg Leu Ser 45 (2) INFORMATION FOR SEQ ID NO: ₹3: (i) SEQUENCE CHARACTERISTICS (A) LENGTH: 4 amino acids (B) TYPE: amino acid 50 (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53: -141-

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Ser His Val Leu
      (2) INFORMATION FOR SEQ ID NO:54:
 5
         (i) \SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
10
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
       His Ser Arg Leu
         1
15
      (2) INFORMATION FOR SEQ ID NO:55:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
              (B) TYPE: amino acid
20
             (D) TOROLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
       Ala Val Asp Phe
      (2) INFORMATION FOR SEQ ID NO:56:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: \4 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY ! linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
35
       Ser Leu Gly Glu
40
      (2) INFORMATION FOR SEQ\ID NO:57:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amin acids
             (B) TYPE: amino acid
45
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION SEQ ID NO:57:
       Ala Val Thr Leu
50
      (2) INFORMATION FOR SEQ ID NO: $8:
                                      -142-
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(i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
 5
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
       Leu Leu Glu Gly
         1
10
      (2) INFORMATION FOR SEQ ID NO:59:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
             (B) TAYPE: amino acid
15
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEO ID NO:59:
20
       Leu Ser Ser Leu
         1
      (2) INFORMATION\FOR SEQ ID NO:60:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
       Leu Gly Gln Leu
      (2) INFORMATION FOR SEQ ID NO:61:
35
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
             (B) TYPE: amino \acid
40
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
       Cys Leu Ser Ser
45
         1
      (2) INFORMATION FOR SEQ ID NO:62:
         (i) SEQUENCE CHARACTERISTICS:
50
             (A) LENGTH: 4 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear
```

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(x \frac{1}{2}) SEQUENCE DESCRIPTION: SEQ ID NO:62:
       Leu Leu Gly Gln
         1
 5
      (2) INFORMATION FOR SEQ ID NO:63:
         (i) SEQUENCE CHARACTERISTICS:
             (A)\ LENGTH: 4 amino acids
                 \TYPE: amino acid
10
             (B)
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
15
       Ser Ser Leu Leu
         1
      (2) INFORMATION FOR SEQ ID NO:64:
         (i) SEQUENCE CHARACTERISTICS:
20
             (A) LENGTH: 4 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
       Gly Gln Leu Ser
      (2) INFORMATION FOR SEQ ID NO:65:
30
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
       Leu Gln Ser Leu
40
      (2) INFORMATION FOR SEQ ID NO:66:
         (i) SEQUENCE CHARACTERISTICS:
45
             (A) LENGTH: 4 amino actids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
50
       Leu Gly Thr Gln
         1
```

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(2) \INFORMATION FOR SEQ ID NO:67:
             SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
             (B) TYPE: amino acid
5
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
       Ala Leu Gln Ser
10
         1
      (2) INFORMATION FOR SEQ ID NO:68:
         (i) SEOUENCE CHARACTERISTICS:
15
             (A) LENGTH: 4 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
20
       Leu Leu Gly Thr
         1
      (2) INFORMATION FOR SEQ ID NO:69:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH 1 4 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear
30
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
       Asn Ala Ile Phe
35
         1
      (2) INFORMATION FOR SEQ ID NO:70:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 4 amino acids
40
             (B) TYPE: amino adid
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
45
       Leu Ser Phe Gln
      (2) INFORMATION FOR SEQ ID NO:71:
50
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 22 amino actids
                                      -145-
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	(B) TYPE: amino acid (D) TOPOLOGY: linear
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
	Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu 1 10 15
10	Leu Arg Asp Ser His Val Leu 20 22
	(2) INFORMATION FOR SEQ ID NO:72:
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 amino acids (B) TYPE amino acid (D) TOPOLOGY: linear
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
	His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr 1 10 15
	Pro Val Leu Pro Ala Val Asp Phe 24
7	(2) INFORMATION FOR SEQ ID NO:73:
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
y .	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
35	Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln 1 5 10 15
40	Asp Ile Leu Gly Ala Val Thr Leu 20 23
	(2) INFORMATION FOR SEQ ID NO 74:
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
50	(xi) SEQUENCE DESCRIPTION: SEQ D NO:74:
	Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr 1 5 10 15
	110

	Cys Deu Ser Ser Leu Leu 20 21	
5	(2) INFORMATION FOR SEQ ID NO:75:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
15	Gly Gln Leu\Ser Gly Gln Val Arg Leu Leu Gly Ala Leu Gl	ln 15
13	Ser 16	
20	(2) INFORMATION FOR SEQ ID NO:76:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH 22 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
3 h	Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala Hi	is 15
	Lys Asp Pro Asn Ala Ile Phe 20 22	
el i	(2) INFORMATION FOR SEQ ID NO:77:	
35 40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
45	Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Me	et 15
	Leu Val Gly Gly Ser Thr Leu Cys Val Arg 20 25	